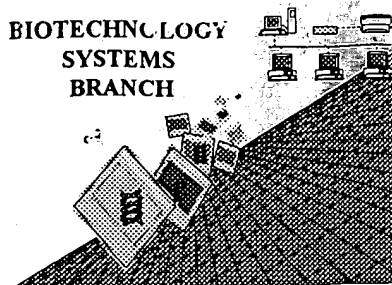


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 08/653,294B

Source: 1644

Date Processed by STIC: 6/26/2001

RECEIVED

JUL 11 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RECEIVED¹⁶⁴⁴

JUL 11 2001

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/653,294B

DATE: 06/20/2001

TIME: 11:11:44

TECH CENTER 1600/2900

Input Set : D:\28600-20200.txt

Output Set : N:\CRF3\06202001\H653294B.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Stanford University
 4 Clayberger, Carol
 5 Krensky, Alan
 6 Buelow, Roland
 8 <120> TITLE OF INVENTION: IMMUNOMODULATING DIMERS
 11 <130> FILE REFERENCE: 28600-20200.23
 13 <140> CURRENT APPLICATION NUMBER: 08/653,294B
 14 <141> CURRENT FILING DATE: 1996-05-24
 16 <150> PRIOR APPLICATION NUMBER: US 08/222,851
 17 <151> PRIOR FILING DATE: 1994-04-05
 19 <150> PRIOR APPLICATION NUMBER: US 07/844,716
 20 <151> PRIOR FILING DATE: 1992-03-02
 22 <150> PRIOR APPLICATION NUMBER: US 07/755,584
 23 <151> PRIOR FILING DATE: 1991-09-03
 25 <150> PRIOR APPLICATION NUMBER: US 07/672,147
 26 <151> PRIOR FILING DATE: 1991-03-19
 28 <150> PRIOR APPLICATION NUMBER: US 07/561,246
 29 <151> PRIOR FILING DATE: 1990-07-30
 31 <150> PRIOR APPLICATION NUMBER: US 07/008,846
 32 <151> PRIOR FILING DATE: 1987-01-30
 34 <160> NUMBER OF SEQ ID NOS: 42
 36 <170> SOFTWARE: FastSEQ for Windows Version 4.0

pp 1-3
 Please
 consult
 Sequence Rules,
 for valid
 format

RECEIVED
 DEC 20 2001
 TECH CENTER 1600/2900

ERRORED SEQUENCES

38 <210> SEQ ID NO: 1
 39 <211> LENGTH: 10
 40 <212> TYPE: PRT
 41 <213> ORGANISM: Human
 43 <220> FEATURE:
 44 <221> NAME/KEY: VARIANT Xaa at location 2
 45 <222> LOCATION: (1)...(10)
 46 <223> OTHER INFORMATION: Xaa76 = E or V;
 47 Xaa77 = D, S or N;
 48 Xaa79 = R or G;
 49 Xaa80 = I or N;
 W--> 50 Xaa81 is a hydrophobic or small amino acid;
 W--> 51 Xaa82 = R or L;
 W--> 52 Xaa83 = G or R;
 W--> 53 Xaa84 = is a hydrophobic or small amino acid.
 55 <400> SEQUENCE 1
 56 Arg Xaa76 Xaa77 Leu Xaa79 Xaa80 Xaa81 Xaa82 Xaa83 Xaa84
 E--> 57 1 5 10
 59 <210> SEQ ID NO: 2
 60 <211> LENGTH: 10
 61 <212> TYPE: PRT

Reword the statement:

Xaa at location 2

is

Xaa76 = E or V;

Per 1.823 of Sequence Rules,
 the maximum number of
 lines in <223> response is
 4; insert a <220> after the
 4th line and insert <223> at
 beginning of 5th line

invalid - do not
 insert numbers next to
 Xaa's; just show
 Xaa

misaligned amino
 acid nos - see
 item 3 on error
 summary sheet

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/653,294B

DATE: 06/20/2001

TIME: 11:11:44

Input Set : D:\28600-20200.txt

Output Set: N:\CRF3\06202001\H653294B.raw

RECEIVED

JUL 11 2001

TECH CENTER 1600/2900

62 <213> ORGANISM: Human
64 <220> FEATURE:
65 <221> NAME/KEY: VARIANT
66 <222> LOCATION: (1)...(10)
67 <223> OTHER INFORMATION: Xaa76 = E or V;
68 Xaa77 = D, S or N;
69 Xaa79 = R or G;
70 Xaa80 = I or N;
W--> 71 Xaa81 is a hydrophobic or small amino acid;
W--> 72 Xaa82 = R or L;
W--> 73 Xaa83 = G or R;
W--> 74 Xaa84 = is a hydrophobic or small amino acid.
76 <400> SEQUENCE: 2
E--> 77 Xaa84 Xaa83 Xaa82 Xaa81 Xaa80 Xaa79 Leu Xaa77 Xaa76 Arg
E--> 78 1 5 10 *misaligned nos.*
80 <210> SEQ ID NO: 3
81 <211> LENGTH: 10 *9 shown*
82 <212> TYPE: PRT
83 <213> ORGANISM: Human
85 <220> FEATURE:
86 <221> NAME/KEY: VARIANT
87 <222> LOCATION: (1)...(10)
88 <223> OTHER INFORMATION: Xaa1 = Any Amino Acid;
89 Xaa2 = N or I; or any amino acid of at least five carbon atoms;
90 Xaa3 = I or hydrophobic or small amino acid;
91 Xaa4 = R or any aliphatic amino acid of at least five carbon atoms;
W--> 92 Xaa5 = G or R or any aliphatic amino acid;
W--> 93 Xaa6 = any amino acid, hydrophobic or small.
95 <400> SEQUENCE: 3
96 Arg Glu Xaa1 Leu Arg Xaa2 Xaa3 Xaa4 Xaa5
E--> 97 1 5 10
433 <210> SEQ ID NO: 38
434 <211> LENGTH: 10
435 <212> TYPE: PRT
436 <213> ORGANISM: Human
438 <220> FEATURE:
439 <221> NAME/KEY: VARIANT
440 <222> LOCATION: (1)...(10)
441 <223> OTHER INFORMATION: Xaa77 = D, S or N;
442 Xaa80 = I or N;
443 Xaa81 = A or L;
444 Xaa82 = R or L;
W--> 445 Xaa83 = G or R.
447 <400> SEQUENCE: 38
E--> 448 Arg Glu Xaa77 Leu Arg Xaa80 Xaa81 Xaa82 Xaa83 Tyr.
E--> 449 1 5 10 *misaligned nos.*
451 <210> SEQ ID NO: 39
452 <211> LENGTH: 10
453 <212> TYPE: PRT

same error

TECH CENTER 1600/2900

DEC 20 2001

RECEIVED

*same error**same error*

RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/08/653,294B

TIME: 11:11:44

Input Set : D:\28600-20200.txt

Output Set: N:\CRF3\06202001\H653294B.raw

454 <213> ORGANISM: Human

456 <220> FEATURE:

457 <221> NAME/KEY: VARIANT

458 <222> LOCATION: (1)...(10)

459 <223> OTHER INFORMATION: Xaa77 = D,S or N;

460 Xaa80 = I or N;

461 Xaa81 = A or L;

462 Xaa82 = R or L;

W--> 463 Xaa83 = G or R.

465 <400> SEQUENCE: 39

E--> 466 Tyr Xaa83 Xaa82 Xaa81 Xaa80 Arg Leu Xaa77 Glu Arg ,

E--> 467 1 5 10

VERIFICATION SUMMARY

PATENT APPLICATION: US/08/653,294B

DATE: 06/20/2001

TIME: 11:11:45

Input Set : D:\28600-20200.txt

Output Set: N:\CRF3\06202001\H653294B.raw

L:50 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:51 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:52 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:53 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:57 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:57 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:1
L:71 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:72 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:73 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:74 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:77 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:77 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:78 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:92 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:93 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:97 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:97 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:3
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:445 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:448 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:448 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:449 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
L:463 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:466 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:466 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:466 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:467 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39